AD128804 RESULT

ADI28804 standard; protein; ADI28804;

123

(first entry) 22-APR-2004

domain K77Q/K82Q mutant PIN1 peptidyl-prolyl isomerase

gene; mutan Human; PIN1; peptidyl-prolyl isomerase; enzyme;

Homo sapiens

Synthetic

Location/Qualifiers 5 Misc-difference

"Encoded by GC" note≕ Misc-difference

"Wild-type Lys substituted by "Wild-type Lys substituted by note= /note= 42 Misc-difference

Gln"

WO2004005315-A2

15-JAN-2004

27-JUN-2003; 2003WO-IB003101

09-JUL-2002; 2002US-0394889P

PFIZER INC ~

HOH Zhu ບັ Parge HE, Gno ഗ Gaur Ferre RA, Ga Nakayama GR, Dagostino EF, Mroczkowski B, Matthews DA, Margosiak S,

2004-099367/10

N-PSDB; ADI28803

domain useful and design of Novel polypeptide containing PIN1 peptidyl-prolyl isomerase for drug discovery and for designing for the identification modulators of PIN1 peptidyl-prolyl isomerase activity.

English. 63pp; 4, Claim 7; SEQ ID NO

The present sequence is the coding sequence of a mutated peptidyl-prolyl isomerase (PPIase) domain of human PINI, corresponding to amino acids 45-163 of full-length PINI. The mutations result in substitution of Gln residues for the native Lys-77 and Lys-82 amino acid residues of the PPIase domain. Lys-77 and Lys-82 comprise the active site of the PPIase domain. PINI is a phosphorylation-dependent PPIase and a regulator of Cdc25. The invention relates to mutant PINI WW domain, and to the PPIase domain but not containing the PINI WW domain, and to the PPIase domain but not containing the PINI WW domain, and to the PPIAse soft these polypeptides and to the X-ray crystal structures of the mutant PINI PPIase polypeptides and small entities that bind to the PINI PPIase substrate-binding domain. The structure coordinate data derived from these crystals provides a three-dimensional description of the substrate-binding site of PINI PPIase useful in drug discovery and design for the identification and design of modulators of PINI PPIase 

Sequence 123 AA;

Gaps ; 0 Length 123; Indels .. 0 Score 526; DB 8; Pred. No. 1.5e-51; ; Mismatches ( 2; 98.5%; ilarity 98.1%; Conservative Similarity 103; Query Match .Local Matches Best

1 HLLVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKSGEEDFESLASQFSDCSSAKA

78 RGDLGAFSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHIILRTE 19 61 ద ð

RESULT 1: ABG12572

standard; protein; 191 ABG12572

**ABG12572** 

entry) (first 18-FEB-2002

diagnostic protein Novel human

forensic; disorder. mapping; gene mapping; gene therapy; medical imaging; diagnostic; genetic chromosome food supplement; Human;

Homo sapiens

WO200175067-A2

11-OCT-2001

Skr. Did Sc

2001WO-US008631 30-MAR-2001;

2000US-00540217 2000US-00649167 31-MAR-2000; 23-AUG-2000;

(HYSE-) HYSEQ INC

Tang YT; Liu C, Drmanac RT,

WPI; 2001-639362/73 N-PSDB; AAS76759.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 42931; 103pp; English

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites polypeptide and polynucleotide sequences have applications in the printed sequence deta for this amino acid sequences. Abgonolo-Abg30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 191

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Gaps .. 7 Length 191; Indels .. '. Score 453; DB 4; Pred. No. 5.2e-43; ; Mismatches 5; Similarity 89.4%; 33; Conservative 93; Ouery Match Best Local Matches 9

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analyzed for minates many ed with known represent tic tissue a entified by ptides (I) eatment of Gaps optionally olate full-ction of (I Rosenthal This invention describes novel nucleic acid sequences (A) that expressed at high level in normal prostatic tissue. Polypeptide encoded by (A) are used: (a) for identifying agents for treatme prostatic cancer and (b) for therapy of prostate cancer, option expressed by gene therapy methods. (A) is also used to isolate length genes (for gene therapy) and for recombinant production which can be used to raise specific antibodies. (A) are identificantly of ESTs (expressed sequence tags) before these are ansexpression pattern (therapy). This approach eliminat the false results, as regards tissue specificity, associated winethods that use single (usually short) ESTs. AAY48304-Y48456 repetides encoded by the expressed sequence tags described in the of the invention ö 26 102 RGDLGAFSRGOMOKPF-EDASFALRT-GEMSGPVFTDSGIHIIL 102 ||||||:|||||||||| |RGDLGSFSRGOMOKPFXRTPRFALRTGGDERGPCFTDSGIHIIL 172 at high level in normal prostate to treat cancer and screen for Length 163 d sequence tag; EST; prostate; tumor; treatment; tissue specificity; human. 回 Indels Dahl Score 416; DB 2; I Pred. No. 6.9e-39; ); Mismatches 4; ບ Human prostate cancer-associated protein 74. Pilarsky (META-) METAGEN GES GENOMFORSCHUNG MBH Schmitt A, standard; protein; 163 ; 0 Claim 25; 152; 194pp; German. 98DE-01011194 98DE-01011194 77.9%; ilarity 95.3%; Conservative C New nucleic acid expressed encoded polypeptides, used (first entry) Hinzmann B, WPI; 1999-519629/44 N-PSDB; AAZ33510. Expressed sequence l Similarity 82; Conserv Sequence 163 AA; DE19811194-A1 110 MAR-1998; Homo sapiens 10-MAR-1998; 08-DEC-1999 16-SEP-1999 AAY48377; 129 61 AAY48377 E cancer; Query Match Best Local agents. Specht Matches RESULT AAY4837 ID AA Z DP δ a a 

standard; protein; 141

ADP29953;

ADP29953

RESULT ADP2995

SQFSDCSSAKA

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144

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SQFSDCSSAKA